101579356

AP20Rec'd FJIFTO 12 MAY 2006

<110>	Gregor, Polly Concetti, Antonio Houghton, Alan Venanzi, Franco Maria
<120>	Compositions and Methods for Synergistic
	Induction of Antitumor Immunity
<130>	D6547
<141>	2006-05-12
<150>	PCT/US2004/038022
<151>	2004-11-15
<160>	13
<210>	1
<211>	5220
<212>	DNA
<213>	artificial sequence
<220>	
<223>	nucleotide sequence for mouse TEM8
<400>	1
	tcgactgcaa agcttcaagc gcagcctggg agcggcctgg 50 ccggcagctc cacacagcag aacgccctgg gtccctgaaa 100
	gggctcagaa ccagcggaaa ccaaagcgaa atccttgaac 150
	aattgcttcc gggcgtttgc tgagagccgg gggacctgac 200
	gccgcgtatg gcgcgccct gatgtcacac ggacgccagc 250
	ctccggctgc agcatggacc gcgcggggcg cctgggtgcg 300
	gactctgcgt ggctgcactc gtgctcgtgt gcgccggaca 350 cgcgaggatg gggaccagc ttgctacgga ggattcgacc 400
	cgcgaggatg ggggaccagc ttgctacgga ggattcgacc 400 cctggacaag tcaggaagtg tgctgcacca ctggaatgaa 450
•	

```
500
atctactact tcgtggagca gttggctcat agattcatca gcccacagct
                                                        550
aaggatgtcc ttcattgtct tctctactcg agggacaact ttaatgaaac
taactgagga cagggaacag atccgacaag gcctagaaga gctccagaaa
                                                        600
                                                        650
gttctgccag gaggagacac ttacatgcac gaaggattcg agagggccag
tgagcagatt tactatgaga acagtcaagg atacaggacg gcgagcgtca
                                                        700
                                                        750
tcatcqcqtt qacqqatqqq gaqctqcacq aggacctctt cttctactca
                                                        800
gagagggagg ctaaccgatc ccgagacctt ggtgcgattg tttactgcgt
tggcgtgaag gatttcaatg aaactcagtt ggctcggatt gcagacagta
                                                        850
                                                        900
aggaccacgt gtttcctgtg aacgacggct tccaggctct ccaaggcatt
atccactcaa ttttaaagaa atcctgcatc gaaattctgg cggctgaacc
                                                        950
atccaccatc tgcgcgggag agtcctttca agtggtcgta agaggaaatg 1000
gcttccgaca tgcccgcaat gtggacaggg tcctctgcag cttcaaaatc 1050
aatgactcag tcacgctcaa tgagaagccc tttgctgtgg aagacactta 1100
tttgctgtgc ccagcaccaa tcttgaaaga agttggcatg aaagctgcac 1150
tgcaggtcag catgaacgac ggcctgtcct tcatctccag ttctgtcatc 1200
atcaccacca cacactgttc agacggctcc atcctggcga ttgctctgct 1250
ggtcctcttc ctgctgctgg ccctggcgct gctctggtgg ttctggcccc 1300
tctgctgcac agtgatcatc aaggaggtcc ctccaccccc tgttgaggag 1350
agtgaggaag aagacgatga tggtttgcca aagaagaaat ggcccacagt 1400
agatgcctct tattatggtg gacgcggtgt gggaggcatt aaaagaatgg 1450
aggtccgctg gggagaaaag ggctccacag aagaaggggc gaagttagaa 1500
aaggcaaaga atgcacgagt caagatgcca gagcaagaat atgagttccc 1550
agaaccccga aacctcaaca acaacatgcg ccggccttcc tcgcctcgga 1600
agtggtactc gcccatcaag ggaaaactcg atgccttgtg ggttctgctg 1650
agaaaaggat atgaccgagt gtctgtgatg aggccacagc caggagacac 1700
gggacgctgt atcaacttca ccagagtgaa gaacagtcag ccagccaagt 1750
atcccctgaa caacacctac caccccagct ccccacctcc cgctcctatc 1800
tacacaccc cacccctgc tecccactgc cetececcag ceeccagtgc 1850
ccccactcct cccattcctt ccccaccatc cactctcccc cctcctcctc 1900
aggececace cectaacagg geacetecee cetecegace tectecaagg 1950
ccttctgtct agaacccaaa gtccgagctc tgggctgcct gagcaactcc 2000
agcaggaggc ttctctgctg aaagaaagat ctgcccagcc tatgtggtga 2050
gtggcggctg atgtttgcac gatttaaaag caagtcgtga tgggcagaac 2100
aaaatgggca ttttgaactg cctgaagaca gacaatgaga caataacagt 2150
cacattatag cctgtgaccc ctcacctcta gaggaaggtt cccgagatgg 2200
ccacattgcc acagtgctct cagccagatt atgtcccatg aagaccagga 2250
agaaagtgac ttccaagaat ggaatgcagc attggataag aaacacctgg 2300
ctgagattct gacctcactg atttgactct tgattcttgg actgggagcc 2350
aggccatctc caccctggt accacccagc aactctgaaa atgtgcagtg 2400
tccctagtat gcatcgaata ggtatccaac tgggatctgc aggttgcctt 2450
ataaagagca tatgctctat tctctttccc gaacttcctg gtttcccagt 2500
gatgagggaa ggggaaaggt gttgccatgc ttagaagtta gaggacgtca 2550
gtgctcagca ctgatggaga agcgttgatg ggagtgtcca gctcttacat 2600
ctagaaatgg ctggcttcag caggcacagt tcctaaacca acaagccttg 2650
tcattgtcaa aggcaaccta ctaatgattc accttaaaca tcaaggttga 2700
ctgtggcata ggtcagagct gatcacacag aaccttcccc atgaaatcgc 2750
aaggttcctc atcttcaaat acccaggacc ccagagattt ctaaatccag 2800
```

ctaagagaca gtagtcctga cttggcaaga aaaccattcc cagttgtttt 2850 actctgaaac aggccgttgt atgtatggta tatctctcct tggcctttca 2900 acctgctcac aagtattacc agttatgaag caaggagaaa tacatccagt 2950 gtgtaataga aaagetetge ceacaateee catgteacte etetacatta 3000 ttctgaagct gcttggtcag tgagcccttt aacctcatgt agactctgga 3050 cactgtcacc caatcatgaa aacagaggtc attgtcaaag gcagtgtata 3100 gcctgtacaa aaatgatgct tccttcctca gtttccacag gccccaaaat 3150 tcctgtctta ggctcctaaa cctctaaact ttttcctgga acaaaagata 3200 taaaacgggc ataagttttt atgttttggg ctgtgatctc caaagatcct 3250 tcaagaactc aagttagcct cattcttcca gcttgtttag aacagaggca 3300 tccaggtgtc atgcactcca tagacaccaa tccttgttcc caaggcagac 3350 attattaatc aatctcagca ctagttctca atttaatcca attatatttt 3400 tccacagtac ttcacatctc ttatgacctg ttggtcatca gttagaattg 3450 agagagataa acactgtttg taatccctac cttagaaaga aaagcagagg 3500 agaatggggg aaccaccagc ataaaagtta ttatctgggg aaaatcgacc 3550 tgaaagaacg cccaagtcca agacctatgg tgctgacacc aaagtaacac 3600 tttcccaagt gtaccccaga ccccactctt ctccctgtgg ccaccactcc 3650 ctgcttttca ggagttgtga aaaagatctc cttcaccctt actgtgcccc 3700 catattagaa caaggcttgt ttagtgtagt ccttgttaaa caggtgccag 3750 aatgtctcag ccacctgaga tgacattgct gggccccaga aaaccattcc 3800 aaggagaatg ggctccccag gctcagagca tgcaactatg agcccatggc 3850 aactgttttg actgctggca gtacaaaacg ggccacccca cattacagct 3900 gcaggatttg tgcagccata agaaagtatg aaccaagatg ctggtgttgc 3950 tgttcaacaa gcatgggctt cggggaaggc agcagactcc gagagcaggc 4000 cttgtgcagt gtcccaaggg gctgtggtga agtgtctgag gaaaaatgaa 4050 tgctgataca tggtgattct gagaagaatt tgcaaggttt gaccttagaa 4100 tttatggaat gtcttccctg gtcattcaga attatggcta gaagtttcta 4150 gaaaccgtca aggttaatac ctttcagagt aggtgattac aggcaggaag 4200 agetttgatg tggtttacaa ageceateag ttetgtgtea tteeetgtaa 4250 gcaacaggag atggttggttg tgattagcaa actgcatgtg ttatttgttt 4300 gactccttgt tattgtcctt acggaggatt ttttttatat aagccaaatt 4350 ttgttgtata tattcatatt ccacgtgaca gatggaagca cgtcctatca 4400 gtgtgaataa aaagaacagt tgtagtaaat tattaaagcc agtgatttca 4450 tggcaggtta ccctaccaag ctgtgcttgt tgatctccca tgaccatact 4500 gcttttacaa tgtacaaata gttcctaggt gacgagaccc tcctttacat 4550 aatgccgatg acagccttgc tgggaactgc ggtccttctg ctgtgacagc 4600 cagctcgaaa acaggtcctg cctggagctt gccacacact ttagggagac 4650 ataagagetg tettteecea gegteaggga caaagetace ataaagaagt 4700 ggaaaagtet tggeteteea geetgggaea gaggtetete tggaaceeca 4750 aggaagagca gaaatgatcc ttgcctgcca ctgcacacaa tgtgatggtg 4800 gaaaatccat caaggaataa ttgtgagata atgaccgaca gttcaggcgc 4850 aaagggaatt catgctgtgt aaagtgggtg gaattcgttt gcaagctatg 4900 caaagcctga tcttactcac caggaggatg gaaagggttt ttttagttat 4950 ctgagctcag ctgagttatc acgcttggag aaccgattta aaggaattag 5000 aatatgattt ctgaatacac ataacattaa actcttctct ttttctatgg 5050 taatttagtt atggacgttc agcgtctctg agttattgtt ataaaagact 5100 tgtcatcacc gcactgtgct gtaggagact gggctgaacc tgtacaatgg 5150

```
<210>
               2
     <211>
               561
     <212>
               PRT
     <213>
               artificial sequence
     <220>
     <223>
               amino acid sequence for mouse TEM8
     <400>
Met Asp Arg Ala Gly Arg Leu Gly Ala Gly Leu Arg Gly Leu Cys
Val Ala Ala Leu Val Leu Val Cys Ala Gly His Gly Gly Arg Arg
                 20
                                      25
Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe
                 35
                                      40
Ile Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile
                 50
                                      55
Tyr Tyr Phe Val Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln
                 65
                                      70
Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu
                                      85
Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu
                 95
                                     100
Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu
                110
                                     115
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Ser Gln
Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu
                140
Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg
                155
                                     160
Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp
                170
                                     175
                                                          180
Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His
                185
                                     190
                                                          195
Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile
                200
                                     205
His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu
```

```
220
                215
Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Arq
                                    235
Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys
                                    250
                245
Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
                                    265
Ala Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys
                                                         285
                275
                                    280
Glu Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly
                290
                                     295
Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr Thr His Cys
                                     310
                305
Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Val Leu Phe Leu
                                     325
                320
Leu Leu Ala Leu Ala Leu Trp Trp Phe Trp Pro Leu Cys Cys
                                     340
                335
Thr Val Ile Ile Lys Glu Val Pro Pro Pro Val Glu Glu Ser
                350
                                     355
                                                         360
Glu Glu Glu Asp Asp Gly Leu Pro Lys Lys Trp Pro Thr
                                                         375
                                     370
                365
Val Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Gly Ile Lys
                                                         390
                                     385
                380
Arg Met Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu Glu Gly
                                                         405
                                     400
                395
Ala Lys Leu Glu Lys Ala Lys Asn Ala Arg Val Lys Met Pro Glu
                                                         420
                                     415
                410
Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn Asn Met
                                     430
Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile Lys Gly
                440
Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp Arg
Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Arg Cys Ile Asn
                470
                                     475
Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
                485
                                     490
Asn Thr Tyr His Pro Ser Ser Pro Pro Pro Ala Pro Ile Tyr Thr
                                     505
                500
Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala
                                     520
                                                         525
                515
Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro
                                     535
                530
Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro
                                                         555
                545
                                     550
Pro Pro Arg Pro Ser Val
                560
```

```
<211>
               252
     <212>
               PRT
               artificial sequence
     <213>
     <220>
               amino acids 27-279 for mouse TEM8
     <223>
     <400>
Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp
Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His Trp
Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Arg Phe Ile
                                      40
                 35
Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly
                 50
                                      55
Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln
                                                           75
                                      70
                 65
Gly Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr
                                                           90
                                      85
Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu
                                     100
Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr
                110
                                     115
                                                          120
Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu
                                     130
Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly
                                     145
                                                          150
                140
Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
                                                          165
                155
Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln
                170
                                     175
Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
                185
Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val
                200
                                     205
                                                          210
Val Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg
                215
                                     220
                                                          225
Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu
```

3

<210>

tatgcgtcgg ccttcttccc cccggaagtg gtactctcca atcaagggaa 1500

aactcgatgc cttgtgggtc ctactgagga aaggatatga tcgtgtgtct 1550 gtgatgcgtc cacagccagg agacacgggg cgctgcatca acttcaccag 1600 ggtcaagaac aaccagccag ccaagtaccc actcaacaac gcctaccaca 1650 cetectegee geetectgee eccatetaea etececeaee teetgegeee 1700 cactgeeete eccegeeece cagegeeect acceeteeca tecegteece 1750 accttccacc cttcccctc ctccccaggc tccacctccc aacagggcac 1800 ctcctccctc ccgccctcct ccaaggcctt ctgtctagag cccaaagttc 1850 ctgctctggg ctctctcaga aacttcagga gatgttagaa caagtctttc 1900 cagttagaga agaggagtgg tgataaagcc cactgacctt cacacattct 1950 aaaaattggt tggcaatgcc agtataccaa caatcatgat cagctgaaag 2000 aaacagatat tttaaattgc cagaaaacaa atgatgaggc aactacagtc 2050 agatttatag ccagccatct atcacctcta gaaggttcca gagacagtga 2100 aactgcaaga tgctctcaac aggattatgt ctcatggaga ccagtaagaa 2150 aatcatttat ctqaaqqtqa aatqcaqaqt tgqataaqaa atacattgct 2200 gggtttctaa aatgctgcct tcctgcctct actccacctc catccctgga 2250 ctttggaccc ttggcctagg agcctaagga ccttcacccc tgtgcaccac 2300 ccaagaaaga ggaaaacttt gcctacaact ttggaaatgc tggggtccct 2350 ggtgtggtaa gaaactcaac atcagacggg tatgcagaag gatgttcttc 2400 tgggatttgc aggtacataa aaaatgtatg gcatcttttc cttgcaaatt 2450 cttccagttt ccaagtgaga aggggagcag gtgtttactg atggaaaagg 2500 tatgttgcta tgttgatgtg taagtgaaat cagttgtgtg caatagacag 2550 gggcgtattc atgggagcat cagccagttt ctaaaaccca caggccatca 2600 gcagctagag gtggctggct ttggccagac atggacccta aatcaacaga 2650 caatggcatt gtcgaagagc aacctgttaa tgaatcatgt taaaaatcaa 2700 ggtttggctt cagtttaaat cacttgaggt atgaagttta tcctgttttc 2750 cagagataaa cataagttga tcttcccaaa ataccatcat taggacctat 2800 cacacaatat cactagtttt ttttgtttgt ttgttttttg tttttttct 2850 tggtaaagcc atgcaccaca gacttctggg cagagctgag agacaatggt 2900 cctgacataa taaggatctt tgattaaccc ccataaggca tgtgtgtgta 2950 tacaaatata cttctctttg gcttttcgac atagaacctc agctgttaac 3000 caaggggaaa tacatcagat ctgcaacaca gaaatgctct gcctgaaatt 3050 tccaccatgc ctaggactca ccccatttat ccaggtcttt ctggatctgt 3100 ttaatcaata agccctataa tcacttgcta aacactgggc ttcatcaccc 3150 agggataaaa acagagatca ttgtcttgga cctcctgcat cagcctattc 3200 aaaattatct ctctctctag ctttccacaa atcctaaaat tcctgtccca 3250 agccacccaa attctcagat cttttctgga acaaggcaga atataaaata 3300 aatatacatt tagtggcttg ggctatggtc tccaaagatc cttcaaaaat 3350 acatcaagcc agcttcattc actcacttta cttagaacag agatataagg 3400 gcctgggatg catttatttt atcaatacca atttttgtgg ccatggcaga 3450 cattgctaat caatcacage actatttcct attaagecea etgatttctt 3500 cacaatcett etcaaattae aatteeaaag ageegeeact caacagteag 3550 atgaacccaa cagtcagatg agagaaatga accctacttg ctatctctat 3600 cttagaaagc aaaaacaaac aggagtttcc agggagaatg ggaaagccag 3650 ggggcataaa aggtacagtc aggggaaaat agatctaggc agagtgcctt 3700 agtcagggac cacgggcgct gaatctgcag tgccaacacc aaactgacac 3750 atctccaggt gtacctccaa ccctagcctt ctcccacagc tgcctacaac 3800 agagtetece ageettetea gagagetaaa accagaaatt tecagaetea 3850

```
tgaaagcaac ccccagcct ctccccaacc ctgccgcatt gtctaatttt 3900
tagaacacta ggcttcttct ttcatgtagt tcctcataag caggggccag 3950
aatatctcag ccacctgcag tgacattgct ggacccctga aaaccattcc 4000
ataggagaat gggttcccca ggctcacagt gtagagacat tgagcccatc 4050
acaactgttt tgactgctgg cagtctaaaa cagtccaccc accccatggc 4100
actgccgcgt gattcccgcg gccattcaga agttcaagcc gagatgctga 4150
cqttqctqaq caacqaqatq qtqaqcatca qtqcaaatgc accattcagc 4200
acatcagtca tatgcccagt gcagttacaa gatgttgttt cggcaaagca 4250
ttttgatgga atagggaact gcaaatgtat gatgattttg aaaaggctca 4300
qcaqqatttq ttcttaaacc qactcaqtqt qtcatccccq gttatttaga 4350
attacagtta agaaggagaa acttctataa gactgtatga acaaggtgat 4400
atcttcatag tgggctatta caggcaggaa aatgttttaa ctggtttaca 4450
aaatccatca atacttgtgt cattccctgt aaaaggcagg agacatgtga 4500
ttatgatcag gaaactgcac aaaattattg ttttcagccc ccgtgttatt 4550
gtccttttga actgtttttt ttttattaaa gccaaatttg tgttgtatat 4600
attcgtattc catgtgttag atggaagcat ttcctatcca gtgtgaataa 4650
aaagaacagt tgtagtaaat tattataaag ccgatgatat ttcatggcag 4700
qttattctac caaqctqtqc ttqttqqttt ttcccatgac tgtattqctt 4750
ttataaatgt acaaatagtt actgaaatga cgagaccctt gtttgcacag 4800
cattaataag aaccttgata agaaccatat tctgttgaca gccagctcac 4850
agtttcttgc ctgaagcttg gtgcaccctc cagtgagaca caagatctct 4900
cttttaccaa agttgagaac agagctggtg gattaattaa tagtcttcga 4950
tatctqqcca tqqqtaacct cattqtaact atcatcagaa tgggcagaga 5000
tgatcttgaa gtgtcacata cactaaagtc caaacactat gtcagatggg 5050
ggtaaaatcc attaaagaac aggaaaaaat aattataaga tgataagcaa 5100
atqtttcaqc ccaatqtcaa cccaqttaaa aaaaaaatta atgctgtgta 5150
aaatggttga attagtttgc aaactatata aagacatatg cagtaaaaag 5200
tctgttaatg cacatcctgt gggaatggag tgttctaacc aattgccttt 5250
tcttgttatc tgagctctcc tatattatca tactcagata accaaattaa 5300
aagaattaga atatgatttt taatacactt aacattaaac tcttctaact 5350
ttcttctttc tgtgataatt cagaagatag ttatggatct tcaatgcctc 5400
tgagtcattg ttataaaaaa tcagttatca ctataccatg ctataggaga 5450
ctgggcaaaa cctgtacaat gacaaccctg gaagttgctt tttttaaaaa 5500
5540
```

```
<210> 5
<211> 564
<212> PRT
<213> artificial sequence
<220>
<223> amino acid sequence for human TEM8
```

<400> Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly 20 Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn 55 Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr 85 Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly 100 95 Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met 115 His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn 135 130 Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp 145 150 Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala 155 Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys 185 190 Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala 215 220 Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val 235 Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val 255 250 245 Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys 270 265 Pro Phe Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile 285 280 275 Leu Lys Glu Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr Thr 310 315 305 His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu 330 320 Phe Leu Leu Ala Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu

```
335
                                    340
                                                         345
Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Ala Glu
                350
                                    355
Glu Ser Glu Glu Glu Asp Asp Gly Leu Pro Lys Lys Trp
                365
                                                         375
                                    370
Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Gly
                380
                                    385
Ile Lys Arg Met Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu
                395
                                    400
                                                         405
Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala Arg Val Lys Met
                410
                                                         420
                                    415
Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn Asn
                425
                                    430
                                                         435
Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile
                                     445
Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr
                455
                                    460
Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
                470
                                    475
                                                         480
Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr
                485
                                    490
Pro Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Ala Pro
                                    505
Ile Tyr Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro
                515
                                    520
                                                         525
Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu
                                    535
                                                         540
Pro Pro Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro
                545
                                    550
                                                         555
Ser Arg Pro Pro Pro Arg Pro Ser Val
                560
```

<210> 6

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> Sense strand oligonucleotide sequence to
 make pVAXXCDneu.

<400> 6

cgcaagcttc atcatggagc tggc 24

<210>	7
<211>	24
<212>	DNA
<213>	artificial sequence
<220>	
<223>	Antisense strand oligonucleotide sequence to
	make pVAXXCDneu.
<400>	
gcagaattct	tatgtcaccg ggct 24
<210>	8
<211>	25
<212>	DNA
<213>	artificial sequence
<220>	
<223>	Sense strand oligonucleotide sequence to
	amplify TEM8 cDNA.
<400>	
ggactctgcg	tggctgcact cgtgc 25
<210>	9
<211>	25
<212>	DNA
<213>	artificial sequence
<220>	

to amplify TEM8 cDNA. <400> 9 agagcagcgc cagggccagc agcag 25 <210> 10 <211> 36 <212> DNA <213> artificial sequence <220> <223> FWKpnIm8 sense strand oligonucleotide sequence to clone 28-278 amino acid sequence of TEM8. <400> 10 gggggtaccg caatgggccg ccgcgaggat ggggga 36 <210> 11 <211> 34 <212> DNA <213> artificial sequence <220> <223> RVEcoRIm8 antisense strand oligonucleotide sequence to clone 28-278 amino acid of TEM8. <400> 11 ggtggaattc ctagcacagc aaataagtgt cttc 34 <210> 12

Antisense strand oligonucleotide sequence

<223>

<211>	55
<212>	DNA
<213>	artificial sequence
<220>	
<223>	attBlbis oligonucleotide sequence to amplify
	TEM8 recombinant protein.
<400>	12
	ttgtacaaaa aagcaggctt gatgggccgc cgcgaggatg 50 55
gggga	
<210>	13
<211>	51
<212>	DNA
<213>	artificial sequence
<220>	
<223>	attB2bis oligonucleotide sequence to amplify
	TEM8 recombinant protein.
<400>	13
ggggaccact c	ttgtacaaga aagctgggtc gcacagcaaa taagtgtctt 50 51